

SEQUENCE LISTING

<110> Johansen, et al.

<120> Method

<130> 674509-2025

<140> 09/722,938

<141> 2000-11-27

<150> PCT/IB 00/01886

<151> 2000-11-24

<150> GB 9927801.2

<151> 1999-11-24

<160> 28

<170> PatentIn version 3.0

<210> 1

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Description of Artificial Sequence: N-terminal sequence

<400> 1

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Leu | Pro | Gln | Lys | Asp | Pro | Gly | Tyr |
| 1 | | | | 5 | | | | 10 | |

<210> 2

<211> 61

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 2

| | | | | | | |
|------------|-----------|------------|------------|------------|------------|----|
| actccatggc | tactttgcc | caaaaggacc | caggttacat | tggtattgac | gtcaacgctg | 60 |
| g | | | | | | 61 |

<210> 3

<211> 107

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 3

cgaaatcgat gttggtacca atccatcttc tgttgaaacc ttgcttcacg gatggcaatc 60
ttgggtcagg cttgtctgga gtaccagcgt tgacgtcaat aacaatg 107

<210> 4
<211> 106
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 4
gattggtacc aacatcgatt tcgtttacgt cgtttacact ccacaagggtg cttgtactgc 60
tttggaacaga gctatggaaa agtgttctcc aggtaccgtc agaatc 106

<210> 5
<211> 106
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 5
ttcaacccaaa ccagtaacgt tgataatagc cttgacacat tcgtcgaaaa cgaagtcttc 60
gtaacagtga ccaccagaaa cgattctgac ggtacctgga gaacac 106

<210> 6
<211> 120
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 6
atcaacgtta ctggtttggt tgaatctggt tacgacgacg atagaggta cttcgtctct 60
tccggtgaca ccaactgggg ttcccttcaag accttggtca gagaccacgg tagagttttg 120

<210> 7
<211> 109
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 7
caaaccgtgc aatctggcca aaataccgtc acctccaccg acaatgtgac caccctaaacc 60

gacggagtaa caggaaccac ctggcaaaac tctaccgtgg tctctgaac 109

<210> 8

<211> 109

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 8

tttggccaga ttgcacggtt tgccagtoga ttggttatcc ggtgttgaag ttgtcgtaa 60

gccagtcttg accgaagact ctgttcttaa gtacgttcac aaggattcc 109

<210> 9

<211> 116

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 9

ggcaaactct tgaagtagta tttggtgata ataccgaagt tacctccacc tccaccagtg 60

tgagcccaaa acaactcacc gtcgttacct tcggaatcct tgtgaacgta ctttaag 116

<210> 10

<211> 118

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 10

caaatactac ttcaaggatt tgccaatgtc tccaagaggt gtcacgctt ctaacttaca 60

cttctcttgg gacggtttca ctagagatgc cttgcaagat ttgttgacta agtacttc 118

<210> 11

<211> 118

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 11

ggaggtatac aagtacataa caaactcttc agctgcttgg tggaagattt ggaacttacc 60

aacagtattc ttccaatcac atctagccaa cttgaagtac ttagtcaaca aatcttgc 118

<210> 12

<211> 96

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12

atcttccatc aggcagctga agagtttggt atgtacttgt atacatccta ctctaacgac 60

gccgagagag aagttgcca agacagacac tatcat 96

<210> 13

<211> 102

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13

gaaaggagcc caaccagcat gaccaccaag agctttggta ggctcgcatg ttttgtagat 60

ctgttcaatg tcagcctcca aatgatagtg tctgtcttgg gc 102

<210> 14

<211> 90

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14

gctgggtggg ctcttttccc tgtagacct agacctagac acacatccaa gacttcttat 60

atgcatgacg agactatgga ctaccctttc 90

<210> 15

<211> 120

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15

aatctggaag tctggaaagt ccttgatcat gtaagcagac ttgtacttac ctctctgatt 60

aggaccggaa ccgttgatag tctcagtcaa agcgtagaaa gggtagtcca tagtctcgtc 120

<210> 16
<211> 108
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 16
gactttccag acttccagat tgatgttatc tggaaatacc ttactgaggt tcttgacggg 60
ttgactagtg ccgaaatgaa ggatgctctt cttcaggttg atatgttc 108

<210> 17
<211> 126
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 17
cttgtcttct tcttgccagt atgtctggta ctgcagtttg atgatgtact ctctctgagc 60
aactgcagta gcatcccaaa caaccttgtg aatctcacca ccgaacatat caacctgaag 120
aagagc 126

<210> 18
<211> 108
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18
acatactggc aggaagaaga caaggatgca gttaacttga agtggattag agacttttac 60
gaggagatgt atgagcctta tgggtggtgt ccagacccta acactcag 108

<210> 19
<211> 111
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 19
ggcaccatac ttaccgttct tccagttggt caagtcaaca tcagggtagt tgaagtagca 60

tcctcaaaa acacctttac cactctcaac ctgagtgtta gggctctggaa c 111

<210> 20
<211> 117
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20
aagaacggta agtatgggtgc cttggaactt tacttttttg gtaacctgaa cagattgatc 60
aaggccaaat ggttgtggga tcctaacgag atcttcacaa acaaacagtc tatecct 117

<210> 21
<211> 78
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21
gaattccgcg gccgcctact atttagtctg cttaggctcc ttaagagggt tagtagggat 60
agactgtttg tttgtgaa 78

<210> 22
<211> 1644
<212> DNA
<213> Artificial

<220>
<223> nucleotide sequence of synthetic Hox gene

<220>
<221> CDS
<222> (1)..(1644)
<223> coding sequence of synthetic HOX gene

<400> 22
atg gct act ttg cca caa aag gac cca ggt tac att gtt att gac gtc 48
Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val
1 5 10 15

aac gct ggt act cca gac aag cct gac cca aga ttg cca tcc atg aag 96
Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys
20 25 30

caa ggt ttc aac aga aga tgg att ggt acc aac atc gat ttc gtt tac 144
Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr
35 40 45

| | |
|---|-----|
| gtc gtt tac act cca caa ggt gct tgt act gct ttg gac aga gct atg | 192 |
| Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met | |
| 50 55 60 | |
| gaa aag tgt tct cca ggt acc gtc aga atc gtt tct ggt ggt cac tgt | 240 |
| Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys | |
| 65 70 75 80 | |
| tac gaa gac ttc gtt ttc gac gaa tgt gtc aag gct att atc aac gtt | 288 |
| Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val | |
| 85 90 95 | |
| act ggt ttg gtt gaa tct ggt tac gac gac gat aga ggt tac ttc gtc | 336 |
| Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val | |
| 100 105 110 | |
| tct tcc ggt gac acc aac tgg ggt tcc ttc aag acc ttg ttc aga gac | 384 |
| Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp | |
| 115 120 125 | |
| cac ggt aga gtt ttg cca ggt ggt tcc tgt tac tcc gtc ggt ttg ggt | 432 |
| His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly | |
| 130 135 140 | |
| ggt cac att gtc ggt gga ggt gac ggt att ttg gcc aga ttg cac ggt | 480 |
| Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly | |
| 145 150 155 160 | |
| ttg cca gtc gat tgg tta tcc ggt gtt gaa gtt gtc gtt aag cca gtc | 528 |
| Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val | |
| 165 170 175 | |
| ttg acc gaa gac tct gtt ctt aag tac gtt cac aag gat tcc gaa ggt | 576 |
| Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly | |
| 180 185 190 | |
| aac gac ggt gag ttg ttt tgg gct cac act ggt gga ggt gga ggt aac | 624 |
| Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn | |
| 195 200 205 | |
| ttc ggt att atc acc aaa tac tac ttc aag gat ttg cca atg tct cca | 672 |
| Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro | |
| 210 215 220 | |
| aga ggt gtc atc gct tct aac tta cac ttc tct tgg gac ggt ttc act | 720 |
| Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr | |
| 225 230 235 240 | |
| aga gat gcc ttg caa gat ttg ttg act aag tac ttc aag ttg gct aga | 768 |
| Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg | |
| 245 250 255 | |
| tgt gat tgg aag aat act gtt ggt aag ttc caa atc ttc cac caa gca | 816 |
| Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala | |
| 260 265 270 | |

| | |
|---|------|
| gct gaa gag ttt gtt atg tac ttg tat aca tcc tac tct aac gac gcc Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala 275 280 285 | 864 |
| gag aga gaa gtt gcc caa gac aga cac tat cat ttg gag gct gac att Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile 290 295 300 | 912 |
| gaa cag atc tac aaa aca tgc gag cct acc aaa gct ctt ggt ggt cat Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His 305 310 315 320 | 960 |
| gct ggt tgg gct cct ttc cct gtt aga cct aga aag aga cac aca tcc Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser 325 330 335 | 1008 |
| aag act tct tat atg cat gac gag act atg gac tac cct ttc tac gct Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala 340 345 350 | 1056 |
| ttg act gag act atc aac ggt tcc ggt cct aat cag aga ggt aag tac Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr 355 360 365 | 1104 |
| aag tct gct tac atg atc aag gac ttt cca gac ttc cag att gat gtt Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val 370 375 380 | 1152 |
| atc tgg aaa tac ctt act gag gtt cct gac ggt ttg act agt gcc gaa Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu 385 390 395 400 | 1200 |
| atg aag gat gct ctt ctt cag gtt gat atg ttc ggt ggt gag att cac Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His 405 410 415 | 1248 |
| aag gtt gtt tgg gat gct act gca gtt gct cag aga gag tac atc atc Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile 420 425 430 | 1296 |
| aaa ctg cag tac cag aca tac tgg cag gaa gaa gac aag gat gca gtt Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val 435 440 445 | 1344 |
| aac ttg aag tgg att aga gac ttt tac gag gag atg tat gag cct tat Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr 450 455 460 | 1392 |
| ggt ggt gtt cca gac cct aac act cag gtt gag agt ggt aaa ggt gtt Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val 465 470 475 480 | 1440 |
| ttt gag gga tgc tac ttc aac tac cct gat gtt gac ttg aac aac tgg Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp 485 490 495 | 1488 |
| aag aac ggt aag tat ggt gcc ttg gaa ctt tac ttt ttg ggt aac ctg | 1536 |

Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu
500 505 510

aac aga ttg atc aag gcc aaa tgg ttg tgg gat cct aac gag atc ttc 1584
Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe
515 520 525

aca aac aaa cag tct atc cct act aaa cct ctt aag gag cct aag cag 1632
Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln
530 535 540

act aaa tag tag 1644
Thr Lys
545

<210> 23
<211> 546
<212> PRT
<213> Artificial

<400> 23

Met Ala Thr Leu Pro Gln Lys Asp Pro Gly Tyr Ile Val Ile Asp Val
1 5 10 15

Asn Ala Gly Thr Pro Asp Lys Pro Asp Pro Arg Leu Pro Ser Met Lys
20 25 30

Gln Gly Phe Asn Arg Arg Trp Ile Gly Thr Asn Ile Asp Phe Val Tyr
35 40 45

Val Val Tyr Thr Pro Gln Gly Ala Cys Thr Ala Leu Asp Arg Ala Met
50 55 60

Glu Lys Cys Ser Pro Gly Thr Val Arg Ile Val Ser Gly Gly His Cys
65 70 75 80

Tyr Glu Asp Phe Val Phe Asp Glu Cys Val Lys Ala Ile Ile Asn Val
85 90 95

Thr Gly Leu Val Glu Ser Gly Tyr Asp Asp Asp Arg Gly Tyr Phe Val
100 105 110

Ser Ser Gly Asp Thr Asn Trp Gly Ser Phe Lys Thr Leu Phe Arg Asp
115 120 125

His Gly Arg Val Leu Pro Gly Gly Ser Cys Tyr Ser Val Gly Leu Gly
130 135 140

Gly His Ile Val Gly Gly Gly Asp Gly Ile Leu Ala Arg Leu His Gly
145 150 155 160

Leu Pro Val Asp Trp Leu Ser Gly Val Glu Val Val Val Lys Pro Val
165 170 175

Leu Thr Glu Asp Ser Val Leu Lys Tyr Val His Lys Asp Ser Glu Gly
180 185 190

Asn Asp Gly Glu Leu Phe Trp Ala His Thr Gly Gly Gly Gly Gly Asn
195 200 205

Phe Gly Ile Ile Thr Lys Tyr Tyr Phe Lys Asp Leu Pro Met Ser Pro
210 215 220

Arg Gly Val Ile Ala Ser Asn Leu His Phe Ser Trp Asp Gly Phe Thr
225 230 235 240

Arg Asp Ala Leu Gln Asp Leu Leu Thr Lys Tyr Phe Lys Leu Ala Arg
245 250 255

Cys Asp Trp Lys Asn Thr Val Gly Lys Phe Gln Ile Phe His Gln Ala
260 265 270

Ala Glu Glu Phe Val Met Tyr Leu Tyr Thr Ser Tyr Ser Asn Asp Ala
275 280 285

Glu Arg Glu Val Ala Gln Asp Arg His Tyr His Leu Glu Ala Asp Ile
290 295 300

Glu Gln Ile Tyr Lys Thr Cys Glu Pro Thr Lys Ala Leu Gly Gly His
305 310 315 320

Ala Gly Trp Ala Pro Phe Pro Val Arg Pro Arg Lys Arg His Thr Ser
325 330 335

Lys Thr Ser Tyr Met His Asp Glu Thr Met Asp Tyr Pro Phe Tyr Ala
340 345 350

Leu Thr Glu Thr Ile Asn Gly Ser Gly Pro Asn Gln Arg Gly Lys Tyr
355 360 365

Lys Ser Ala Tyr Met Ile Lys Asp Phe Pro Asp Phe Gln Ile Asp Val
370 375 380

Ile Trp Lys Tyr Leu Thr Glu Val Pro Asp Gly Leu Thr Ser Ala Glu
385 390 395 400

Met Lys Asp Ala Leu Leu Gln Val Asp Met Phe Gly Gly Glu Ile His
405 410 415

Lys Val Val Trp Asp Ala Thr Ala Val Ala Gln Arg Glu Tyr Ile Ile
420 425 430

Lys Leu Gln Tyr Gln Thr Tyr Trp Gln Glu Glu Asp Lys Asp Ala Val
435 440 445

Asn Leu Lys Trp Ile Arg Asp Phe Tyr Glu Glu Met Tyr Glu Pro Tyr
450 455 460

Gly Gly Val Pro Asp Pro Asn Thr Gln Val Glu Ser Gly Lys Gly Val
465 470 475 480

Phe Glu Gly Cys Tyr Phe Asn Tyr Pro Asp Val Asp Leu Asn Asn Trp
485 490 495

Lys Asn Gly Lys Tyr Gly Ala Leu Glu Leu Tyr Phe Leu Gly Asn Leu
500 505 510

Asn Arg Leu Ile Lys Ala Lys Trp Leu Trp Asp Pro Asn Glu Ile Phe
515 520 525

Thr Asn Lys Gln Ser Ile Pro Thr Lys Pro Leu Lys Glu Pro Lys Gln
530 535 540

Thr Lys
545

<210> 24

<211> 5

<212> PRT

<213> Schwanniomyces occidentalis

<400> 24

Ser Ala Ile Gln Ala

1 5

<210> 25

<211> 5

<212> PRT

<213> Artificial

<220>

<223> synthetic signal sequence

<400> 25

Met Ala Thr Leu Pro

1 5

<210> 26

<211> 4

<212> PRT

<213> Artificial

<220>

<223> synthetic signal sequence

<400> 26

Ala Thr Leu Pro

1

<210> 27

<211> 6

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 27

Lys Arg Glu Ala Glu Ala

1 5

<210> 28

<211> 5

<212> PRT

<213> *Aspergillus oryzae*

<400> 28

Ala Pro Ala Leu Ala

1 5